

1
SEQUENCE LISTING

<110> Kaplan, Aaron
Lieman-Hurwitz, Judy
Rachmilevitch, Shimon
Schatz, Daniella
Mittler, Ron

<120> PLANTS CHARACTERIZED BY ENHANCED GROWTH AND METHODS AND NUCLEIC
ACID CONSTRUCTS USEFUL FOR GENERATING SAME

<130> 26863

<160> 13

<170> PatentIn version 3.2

<210> 1

<211> 4957

<212> DNA

<213> Synechococcus sp.

<400> 1

aagcttggat tgaagcgatc ggggtcaatc ccagcgatga tcctcagttc ctctgatgg	60
tcgatccctt tagcgccaag attgaggatc tgctgcaagg gctggatttc gcctatcccg	120
aggccgtgaa agtgggcgga ttggccagtg gtttgggggc agagtcagcg atcgccagct	180
tgttttttca agaccgacag gtcgatggcg tgattgggct agccctcagt ggcaatgtcc	240
agctgcaggc gatcgtggct cagggctgtc gtccagttgg cccgctttgg catgtggcag	300
cggcggagcg caacattctg cggcaacttc agaccgaaga cgaggaaacc atcgccgcgc	360
tgcaagccct acagtcagtc ctgctgcatc tctccctga attacagcga tcgctctgtg	420
tgggcctggc ctgcaattct ttccaaacgg tattacaacc gggcgacttc ctgatccgta	480
acctgctggg gtttgatccc cgcactggtg ctgtagcaat cggcgatcgc attcgagttg	540
ggcagcggct gcagctgcac gtacgggatg cccagacagc ggcggatgac ctcgagcggc	600
aactggggca atggtgcccg cagcatgcga caaaaccagc agcttccctc ttgttttct	660
gcttggggcg cggcaagccc ttctatcagc aggcgaactt cgagtcgcaa ctgattcagc	720
attacctctc agagctgccc ctgctgggct tttctgttaa tggcgaaatc ggcccgatcg	780
ctggcagcac ctacctgcat ggctacacat cgggtgctggc tttgctgtcg gccaaaactc	840
actagcgcca gcgagacctg attgtcgatc tgctgagcgc gactgtagcg ctggaaatag	900
gcccggacct gagcaggcgc atcgccaag ctgaccgtag tatcaccgtc agccaccccc	960
gcccagaaat tccgcaacat cggcaggaga gcgatcgctt ccgcctccga taaattcaac	1020
ggctcatggg tcaacaggcg gatcaagtac tctgactgcg atcgccatcc attcccgcg	1080
aaaacgtttg taaatcagtc ttgatccggt agcgatcgca cccgacggga ctctagttct	1140
agttgccaac cttcagcggc aggttgtacg gttccgagtc ggtagggatg gggatagctg	1200
accaaggaac cggtcgtgac ttcccagaga gcaccttget gactggtggc ttggatgtgg	1260
aggtggcctg tgaagatcac cgagacgctg cccgcttcga ggattgatcg caattcctcg	1320
gcattttcta agatgtagcg ctgaccaagc ggatgctgct gttgatcggg cagatgctcc	1380
aacacattgt ggtgaatcat caccagcgt tggttagcgg tggaaagtggc gagttcttgt	1440
tgcagccagt tgagttgcgc gcaatcgact cgcgcccgat gcagttgatg gcccgcttca	1500
tcaaaagcga tcgaattcag cgaaaacaga tcgagatccg gtgcgatcgt gcagcgatag	1560
taggggcgat cgctcgtgaa gccaaagtct tgatagagct cgacaaaactc ggccacaccg	1620
gtgcgatcgc gatcgtcgc tgccggcggc atatcgtggt tgcccgccac cacatagacc	1680

ggatagggca	actggcgcaa	ttgttgacgc	agccactgat	ggttttcccg	ctccccgtgc	1740
tgggttaa	ccccggcag	caacaggaag	tccaaatcca	gcgctgccag	ttctgtcagg	1800
atgtgtctca	aagccggaat	gctgcactca	atcaaataga	agcgatggg	atggtgccaa	1860
attgtctgcg	gcagccaat	gtggagatcg	ctcagcagcg	caaatacga	cgctcggttc	1920
attgccatcc	cctcagctat	cgagcccgat	tctaggcgaa	gctaggtcga	gtccgttgtc	1980
ttcagttgca	agcattcatg	gccagagttc	gcgttcggca	gcacgtcaat	ccgctctctc	2040
agaaattcca	agtggtcacg	acttggccgg	attggcaaca	ggtctatgcg	gactgcgac	2100
gcccgtgca	tttgatatt	ggctgtgctc	gcgggcgctt	tctgctggca	atggcgacac	2160
gacaacctga	gtggaattat	ctggggctgg	aaattcgtga	gccgctggta	gatgaggcga	2220
acgcgatcgc	ccgcgaacgt	gaactgacca	atctctacta	ccacttcagc	aacgccaat	2280
tggacttgga	accgctgctg	cgatcgctgc	cgacagggat	tttgacggg	gtcagcattc	2340
agttcccgga	tccttggttc	aagaaacgcc	atcaaaagcg	acgcgtcgtc	cagccggaac	2400
tggtgcaagc	cctcgcgact	gcgttacctg	ctgggtcaga	ggtctttctg	caatccgatg	2460
tgctggaagt	gcaggcagag	atgtgcgaac	actttgcggc	ggaaccccg	tttcagcgca	2520
cctgcttgga	ctggctgccg	gaaaatccgc	tgcccgtccc	gaccgagcgc	gaaattgccg	2580
ttcaaaacaa	acagttgcca	gtctaccgtg	ctctcttcat	tcggcagcca	gcggactaag	2640
ctcttaaggc	aagcgttgac	gcgatcgcca	tgactgtctg	gcaaactctg	acttttgccc	2700
attaccaacc	ccaacagtgg	ggccacagca	gtttcttgca	tcggctgttt	ggcagcctgc	2760
gagcttgccg	ggcctccagc	cagctgtttg	tttggtctga	ggcactgggt	ggcttcttgc	2820
ttgctgtcgt	ctacggttcg	gctccgtttg	tgcccagttc	cgccctaggg	ttggggctag	2880
ccgcgatcgc	ggcctattgg	gccctgctct	cgctgacaga	tatcgatctg	cggaagcaa	2940
ccccattca	ctggctgggt	ctgctctact	ggggcgtcga	tgccctagca	acgggactct	3000
cacccgtagc	cgctgcagct	ttagtgggc	tagccaaact	gacgctctac	ctgttggttt	3060
ttgccctagc	ggctcgggtt	ctccgcaatc	cccgtctgcg	atcgctgctg	ttctcggctg	3120
tcgtgatcac	atcgcttttt	gtcagtgtct	acggcctcaa	ccaatggatc	tacggcgttg	3180
aagagctggc	gacttgggtg	gatcgcaact	cggttgccga	cttcacctca	cgggtttaca	3240
gctatctggg	caacccaac	ctgctggctg	cttatctggg	gccgacgact	gccttttctg	3300
cagcagcgat	cggggtgtgg	cgcggctggc	tccccaagct	gctggcgatc	gctgcgacag	3360
gtgcgagcag	cttatgtctg	atcctcacct	acagtcgcgg	tggctggctg	ggttttgcg	3420
ccatgatatt	tgtctgggcg	ttattagggc	tctactgggt	tcaaccccg	ctaccgcac	3480
cctggcgacg	ctggctattc	ccagtcgtat	tggttggaact	agtcgcgggt	ctcttggttg	3540
cgggtgcttg	acttgagccg	ttgcgcgtgc	gcgtgttgag	catctttgtg	gggcgtgaag	3600
acagcagcaa	caacttcggg	atcaatgtct	ggctggcggt	gctgcagatg	attcaagatc	3660
ggccttggtc	gggcacggc	cccgcaata	ccgcctttaa	cctggtttat	cccctctatc	3720
aacaggcgcg	ctttacggcg	ttgagcgctc	actccgtccc	gctggaagtc	gcggttgagg	3780
gcggactact	gggcttgacg	gccttcgctt	ggctgctgct	ggtcacggcg	gtgacggcgg	3840
tgccgcaggt	gagccgactg	cggcgcgac	gcaatcccca	agccttttgg	ttgatggcta	3900
gcttgcccg	tttgccagga	atgctgggtc	acggtctgtt	tgataccgtg	ctctatcgac	3960
cggaaaccag	tacgctctgg	tggtctgtga	ttggagcgat	cgcgagtttc	tggcagcccc	4020
aaccttccaa	gcaactccct	ccagaagccg	agcattcaga	cgaaaaaatg	tagcgggctc	4080

cccaacaaat tcctgtgcac ccgactggat ccaccaccta aactggatcc caaaggtatc 4140
 cgggtgatct agggtcataa cgaactccga ccgcgatcgc gtccgcgaac tgaacctcca 4200
 tcgcaccgaa gcggagttcg ttagtcgttg aagagccaat gctagagggg gctgccgaag 4260
 cagttgggct ggaagcaggc tgcgagaagc caccgcgcatc caaggcaaag ttcagccgac 4320
 cttccgcaaa gactacgatc gccacggcgg ctctgccagc taagtcagcg ctgggttagt 4380
 tgtcatagca gtccgcagac aagttaggac aacttcatag agggactcgc tcagagtcaa 4440
 cagccgctgt ccgtgggggt gcgcaatcac cccacacccc acgcactggg ggactcgact 4500
 cccccaggcc ccccgcaaca agatttcgga taaggggcat cggctgaatc gcgatcgctg 4560
 cgggtaaaaac tagccggtgt tagccatggg tttgagacta atcggcacgg ggcaaaacgt 4620
 cctgatttat ttgctcaatg tgataggtta catcgtcaaa aacaaggccc aagaggtagg 4680
 aaaaatcacg accgccaag tccgagggct ttgctgttg gagcgaccta gggcagacta 4740
 gacagagcat tgctgtgagc caaagcgct tcaattgctg gcggctgtgg gtttttcgga 4800
 gggttccaaa tgaaagacct tttcgtcaat gtccctcgct atccccgcta cttcatcacc 4860
 ttccagctgg gtatttttta gtcgatctac cagtgggtgc ggccgatggt tcgcaaccca 4920
 gtcgcggctt gggcgctgct aggccttgga gtttcga 4957

<210> 2
 <211> 1404
 <212> DNA
 <213> *Synechococcus* sp.

<400> 2
 atgactgtct ggcaaaactct gacttttgcc cattaccaac cccaacagtg gggccacagc 60
 agtttcttgc atcggctggt tggcagcctg cgagcttggc gggcctccag ccagctgttg 120
 gtttggtctg aggcactggg tggtctcttg ctgctgtcg tctacggttc ggctccgttt 180
 gtgccagtt ccgccctagg gttggggcta gccgcgatc cggcctattg ggccctgctc 240
 tcgctgacag atatcgatct gcggcaagca accccattc actggctggt gctgctctac 300
 tggggcgctg atgccctagc aacgggactc tcaccgctac gcgctgcagc tttagttggg 360
 ctagccaaac tgacgctcta cctgttggtt tttgccctag cggctcgggt tctccgcaat 420
 ccccgctcgc gatcgctgct gttctcggtc gtcgtgatca catcgctttt tgcagtgtc 480
 tacggcctca accaatggat ctacggcggt gaagagctgg cgacttgggt ggatcgcaac 540
 tcggttgccg acttcacctc acgggtttac agctatctgg gcaaccccaa cctgctggct 600
 gcttatctgg tgccgacgac tgccttttct cgagcagcga tcgggggtg ggcgggctgg 660
 ctccccaaag tgctggcgat cgctgcgaca ggtgcgagca gcttatgtct gatcctcacc 720
 tacagtcgcg gtggctggct ggggtttgtc gccatgattt ttgtctgggc gttattaggg 780
 ctctactggt ttcaaccccg tctaccgca cctggcgac gctggctatt ccagtcgta 840
 ttgggtggac tagtcgcggt gctcttggtg gcgggtgctt gacttgagcc gttgcgcgtg 900
 cgcgtgttga gcatctttgt ggggcgtgaa gacagcagca acaacttccg gatcaatgtc 960
 tggttgccg tgctgcagat gattcaagat cggccttggc tgggcatcgg ccccggaat 1020
 accgccttta acctggttta tcccctctat caacaggcgc gctttacggc gttgagcgcc 1080
 tactccgtcc cgctggaagt cgcggttgag ggcggactac tgggcttgac ggccttcgct 1140
 tggtgctgc tggtcacggc ggtgacggcg gtgcggcagg tgagccgact gcggcgcgat 1200
 cgcaatcccc aagccttttg gttgatggct agcttggccg gtttggcagg aatgctgggt 1260

```

cacggtctgt ttgataccgt gctctatcga ccggaagcca gtacgctctg gtggctctgt 1320
attggagcga tcgcgagttt ctggcagccc caaccttcca agcaactccc tccagaagcc 1380
gagcattcag acgaaaaaat gtag 1404

```

```

<210> 3
<211> 467
<212> PRT
<213> Synechococcus sp.

```

```

<400> 3

```

```

Met Thr Val Trp Gln Thr Leu Thr Phe Ala His Tyr Gln Pro Gln Gln
1          5          10          15

Trp Gly His Ser Ser Phe Leu His Arg Leu Phe Gly Ser Leu Arg Ala
20          25          30

Trp Arg Ala Ser Ser Gln Leu Leu Val Trp Ser Glu Ala Leu Gly Gly
35          40          45

Phe Leu Leu Ala Val Val Tyr Gly Ser Ala Pro Phe Val Pro Ser Ser
50          55          60

Ala Leu Gly Leu Gly Leu Ala Ala Ile Ala Ala Tyr Trp Ala Leu Leu
65          70          75          80

Ser Leu Thr Asp Ile Asp Leu Arg Gln Ala Thr Pro Ile His Trp Leu
85          90          95

Val Leu Leu Tyr Trp Gly Val Asp Ala Leu Ala Thr Gly Leu Ser Pro
100         105         110

Val Arg Ala Ala Ala Leu Val Gly Leu Ala Lys Leu Thr Leu Tyr Leu
115         120         125

Leu Val Phe Ala Leu Ala Ala Arg Val Leu Arg Asn Pro Arg Leu Arg
130         135         140

Ser Leu Leu Phe Ser Val Val Val Ile Thr Ser Leu Phe Val Ser Val
145         150         155         160

Tyr Gly Leu Asn Gln Trp Ile Tyr Gly Val Glu Glu Leu Ala Thr Trp
165         170         175

Val Asp Arg Asn Ser Val Ala Asp Phe Thr Ser Arg Val Tyr Ser Tyr
180         185         190

Leu Gly Asn Pro Asn Leu Leu Ala Ala Tyr Leu Val Pro Thr Thr Ala
195         200         205

Phe Ser Ala Ala Ala Ile Gly Val Trp Arg Gly Trp Leu Pro Lys Leu
210         215         220

Leu Ala Ile Ala Ala Thr Gly Ala Ser Ser Leu Cys Leu Ile Leu Thr
225         230         235         240

Tyr Ser Arg Gly Gly Trp Leu Gly Phe Val Ala Met Ile Phe Val Trp
245         250         255

```

Ala Leu Leu Gly Leu Tyr Trp Phe Gln Pro Arg Leu Pro Ala Pro Trp
260 265 270

Arg Arg Trp Leu Phe Pro Val Val Leu Gly Gly Leu Val Ala Val Leu
275 280 285

Leu Val Ala Val Leu Gly Leu Glu Pro Leu Arg Val Arg Val Leu Ser
290 295 300

Ile Phe Val Gly Arg Glu Asp Ser Ser Asn Asn Phe Arg Ile Asn Val
305 310 315 320

Trp Leu Ala Val Leu Gln Met Ile Gln Asp Arg Pro Trp Leu Gly Ile
325 330 335

Gly Pro Gly Asn Thr Ala Phe Asn Leu Val Tyr Pro Leu Tyr Gln Gln
340 345 350

Ala Arg Phe Thr Ala Leu Ser Ala Tyr Ser Val Pro Leu Glu Val Ala
355 360 365

Val Glu Gly Gly Leu Leu Gly Leu Thr Ala Phe Ala Trp Leu Leu Leu
370 375 380

Val Thr Ala Val Thr Ala Val Arg Gln Val Ser Arg Leu Arg Arg Asp
385 390 395 400

Arg Asn Pro Gln Ala Phe Trp Leu Met Ala Ser Leu Ala Gly Leu Ala
405 410 415

Gly Met Leu Gly His Gly Leu Phe Asp Thr Val Leu Tyr Arg Pro Glu
420 425 430

Ala Ser Thr Leu Trp Trp Leu Cys Ile Gly Ala Ile Ala Ser Phe Trp
435 440 445

Gln Pro Gln Pro Ser Lys Gln Leu Pro Pro Glu Ala Glu His Ser Asp
450 455 460

Glu Lys Met
465

<210> 4
<211> 1425
<212> DNA
<213> Synechocystis sp.

<400> 4
atggtgtctc ccatctctat ctggcgatcg ctgatgtttg gcggtttttc ccccaggaa 60
tggggccggg gcagtgtgct ccatcgtttg gtgggctggg gacagagttg gatacaggct 120
agtgtgctct ggccccactt cgaggcattg ggtacggctc tagtggcaat aatttttatt 180
gcggctccct tcacctccac caccatgttg ggcattttta tgctgctctg tggagccttt 240
tgggctctgc tgacctttgc tgatcaacca gggaagggtt tgactcccat ccatgtttta 300
gtttttgcct actggtgcat ttcggcgatc gccgtgggat tttctccggt aaaaatggcg 360
gcggcgtcgg ggtagcgaa attaacagct aatttatgtc tgtttctact ggcggcgagg 420
ttattgcaaa acaaacaatg gttgaaccgg ttagtaaccg ttgttttact ggtagggcta 480
ttggtgggga gttacggtct gcgacaacag gtggacgggg tagaacagtt agccacttgg 540

```

aatgacccca cctctacctt ggcccaggcc actaggggtat atagcttttt aggtaatccc      600
aatctcttgg cggcttacct ggtgcccattg acgggtttga gcttgagtgc cctggtggta      660
tggcgacggt ggtggcccaa actgctggga gcaaccatgg tgattgttaa cctactctgt      720
ctctttttta ccagagccg gggcggttgg ctagcagtgc tggccctggg agctaccttc      780
ctggcccttt gttactttctg gtggttacct caattaccca aattttggca acggtggtct      840
ttgcccttgg cgatcgccgt ggcggttata ttaggtgggg gagcgttgat tgcggtggaa      900
ccgattcgac tcagggccat gagcattttt gctgggcggg aagacagcag taataatttc      960
cgcatacaatg tttgggaagg ggtaaaagcc atgatccgag ccgcccctat cattggcatt     1020
ggcccaggta acgaagcctt taaccaaatt tacccttact atatgcggcc ccgcttcacc     1080
gccctgagtg cctattccat ttacctagaa attttgggtg aaacgggtgt agttggtttt     1140
acctgtatgc tctggtctgt ggccgttacc ctaggcaaag gcgtagaact ggtaaacgc      1200
tgtcgccaaa cctcgcccc ggaagccatc tggattatgg gggcttttagc ggcgatcatc      1260
ggtttgttgg tccacggcat ggtagatata gtctgttacc gtccccgggt gagcactttg      1320
tggtggttgc tagtggccat tgttgctagt cagtgggcca gcgccaggc ccgtttggag      1380
gccagtaaag aagaaaatga ggacaaacct cttcttgctt cataa                        1425

```

```

<210> 5
<211> 474
<212> PRT
<213> Synechocystis sp.

```

```
<400> 5
```

```

Met Val Ser Pro Ile Ser Ile Trp Arg Ser Leu Met Phe Gly Gly Phe
1           5           10           15

Ser Pro Gln Glu Trp Gly Arg Gly Ser Val Leu His Arg Leu Val Gly
                20           25           30

Trp Gly Gln Ser Trp Ile Gln Ala Ser Val Leu Trp Pro His Phe Glu
          35           40           45

Ala Leu Gly Thr Ala Leu Val Ala Ile Ile Phe Ile Ala Ala Pro Phe
50           55           60

Thr Ser Thr Thr Met Leu Gly Ile Phe Met Leu Leu Cys Gly Ala Phe
65           70           75           80

Trp Ala Leu Leu Thr Phe Ala Asp Gln Pro Gly Lys Gly Leu Thr Pro
          85           90           95

Ile His Val Leu Val Phe Ala Tyr Trp Cys Ile Ser Ala Ile Ala Val
100           105           110

Gly Phe Ser Pro Val Lys Met Ala Ala Ala Ser Gly Leu Ala Lys Leu
115           120           125

Thr Ala Asn Leu Cys Leu Phe Leu Leu Ala Ala Arg Leu Leu Gln Asn
130           135           140

Lys Gln Trp Leu Asn Arg Leu Val Thr Val Val Leu Leu Val Gly Leu
145           150           155           160

```

Leu Val Gly Ser Tyr Gly Leu Arg Gln Gln Val Asp Gly Val Glu Gln
 165 170 175

Leu Ala Thr Trp Asn Asp Pro Thr Ser Thr Leu Ala Gln Ala Thr Arg
 180 185 190

Val Tyr Ser Phe Leu Gly Asn Pro Asn Leu Leu Ala Ala Tyr Leu Val
 195 200 205

Pro Met Thr Gly Leu Ser Leu Ser Ala Leu Val Val Trp Arg Arg Trp
 210 215 220

Trp Pro Lys Leu Leu Gly Ala Thr Met Val Ile Val Asn Leu Leu Cys
 225 230 235 240

Leu Phe Phe Thr Gln Ser Arg Gly Gly Trp Leu Ala Val Leu Ala Leu
 245 250 255

Gly Ala Thr Phe Leu Ala Leu Cys Tyr Phe Trp Trp Leu Pro Gln Leu
 260 265 270

Pro Lys Phe Trp Gln Arg Trp Ser Leu Pro Leu Ala Ile Ala Val Ala
 275 280 285

Val Ile Leu Gly Gly Gly Ala Leu Ile Ala Val Glu Pro Ile Arg Leu
 290 295 300

Arg Ala Met Ser Ile Phe Ala Gly Arg Glu Asp Ser Ser Asn Asn Phe
 305 310 315 320

Arg Ile Asn Val Trp Glu Gly Val Lys Ala Met Ile Arg Ala Arg Pro
 325 330 335

Ile Ile Gly Ile Gly Pro Gly Asn Glu Ala Phe Asn Gln Ile Tyr Pro
 340 345 350

Tyr Tyr Met Arg Pro Arg Phe Thr Ala Leu Ser Ala Tyr Ser Ile Tyr
 355 360 365

Leu Glu Ile Leu Val Glu Thr Gly Val Val Gly Phe Thr Cys Met Leu
 370 375 380

Trp Leu Leu Ala Val Thr Leu Gly Lys Gly Val Glu Leu Val Lys Arg
 385 390 395 400

Cys Arg Gln Thr Leu Ala Pro Glu Gly Ile Trp Ile Met Gly Ala Leu
 405 410 415

Ala Ala Ile Ile Gly Leu Leu Val His Gly Met Val Asp Thr Val Trp
 420 425 430

Tyr Arg Pro Pro Val Ser Thr Leu Trp Trp Leu Leu Val Ala Ile Val
 435 440 445

Ala Ser Gln Trp Ala Ser Ala Gln Ala Arg Leu Glu Ala Ser Lys Glu
 450 455 460

Glu Asn Glu Asp Lys Pro Leu Leu Ala Ser
 465 470

<210> 6
 <211> 475
 <212> PRT
 <213> Anabaena PCC7120

<400> 6

```

Met Asn Leu Val Trp Gln Arg Phe Thr Leu Ser Ser Leu Pro Leu Lys
1          5          10          15

Gln Phe Leu Ala Thr Ser Tyr Leu His Arg Phe Leu Val Gly Leu Leu
          20          25          30

Ser Ser Trp Arg Gln Thr Ser Phe Leu Leu Gln Trp Gly Asp Met Ile
          35          40          45

Ala Ala Ala Leu Leu Ser Leu Ile Tyr Val Leu Ala Pro Phe Val Ser
          50          55          60

Ser Thr Leu Val Gly Val Leu Leu Ile Ala Cys Val Gly Phe Trp Leu
65          70          75          80

Leu Leu Thr Leu Ser Asp Glu Pro Ser Ser Asn Asn Asn Ser Leu Val
          85          90          95

Thr Pro Ile His Leu Leu Val Leu Leu Tyr Trp Gly Ile Ala Ala Val
          100          105          110

Ala Thr Ala Leu Ser Pro Val Lys Lys Ala Ala Leu Thr Asp Leu Leu
          115          120          125

Thr Leu Thr Leu Tyr Leu Leu Leu Phe Ala Leu Cys Ala Arg Val Leu
130          135          140

Arg Ser Pro Arg Leu Arg Ser Trp Ile Ile Thr Leu Tyr Leu Ser Ala
145          150          155          160

Ser Leu Val Val Ser Ile Tyr Gly Met Arg Gln Trp Arg Phe Gly Ala
          165          170          175

Pro Pro Leu Ala Thr Trp Val Asp Pro Glu Ser Thr Leu Ser Lys Thr
          180          185          190

Thr Arg Val Tyr Ser Tyr Leu Gly Asn Pro Asn Leu Leu Ala Gly Tyr
          195          200          205

Leu Val Pro Ala Val Ile Phe Ser Leu Met Ala Val Phe Val Trp Gln
210          215          220

Gly Trp Ala Arg Lys Ser Leu Ala Val Thr Met Leu Phe Val Asn Thr
225          230          235          240

Ala Cys Leu Ile Phe Thr Tyr Ser Arg Gly Gly Trp Ile Gly Leu Val
          245          250          255

Val Ala Val Leu Gly Ala Thr Ala Leu Leu Val Asp Trp Trp Ser Val
          260          265          270

Gln Met Pro Pro Phe Trp Arg Thr Trp Ser Leu Pro Ile Leu Leu Gly
          275          280          285

```


Gly Leu Ile Gly Val Leu Leu Ile Ala Val Leu Phe Val Glu Pro Val
290 295 300

Arg Phe Arg Val Leu Ser Ile Phe Ala Asp Arg Gln Asp Ser Ser Asn
305 310 315 320

Asn Phe Arg Arg Asn Val Trp Asp Ala Val Phe Glu Met Ile Arg Asp
325 330 335

Arg Pro Ile Ile Gly Ile Gly Pro Gly His Asn Ser Phe Asn Lys Val
340 345 350

Tyr Pro Leu Tyr Gln Arg Pro Arg Tyr Ser Ala Leu Ser Ala Tyr Ser
355 360 365

Ile Phe Leu Glu Val Ala Val Glu Met Gly Phe Val Gly Leu Ala Cys
370 375 380

Phe Leu Trp Leu Ile Ile Val Thr Ile Asn Thr Ala Phe Val Gln Leu
385 390 395 400

Arg Gln Leu Arg Gln Ser Ala Asn Val Gln Gly Phe Trp Leu Val Gly
405 410 415

Ala Leu Ala Thr Leu Leu Gly Met Leu Ala His Gly Thr Val Asp Thr
420 425 430

Ile Trp Phe Arg Pro Glu Val Asn Thr Leu Trp Trp Leu Met Val Ala
435 440 445

Leu Ile Ala Ser Tyr Trp Thr Pro Leu Ser Ala Asn Gln Cys Gln Glu
450 455 460

Leu Asn Leu Phe Lys Glu Glu Pro Thr Ser Asn
465 470 475

<210> 7
<211> 472
<212> PRT
<213> Nostoc punctiforme

<400> 7

Met Asn Leu Val Trp Gln Leu Phe Thr Leu Ser Ser Leu Pro Leu Lys
1 5 10 15

Glu Tyr Leu Ala Thr Ser Tyr Val His Arg Ser Leu Val Gly Leu Leu
20 25 30

Ser Ser Trp Arg Gln Thr Ser Val Leu Ile Gln Trp Gly Asp Ala Ile
35 40 45

Ala Ala Val Leu Leu Ser Ser Ile Tyr Ala Leu Ala Pro Phe Ala Ser
50 55 60

Ser Thr Leu Val Gly Leu Leu Leu Val Ala Cys Val Gly Phe Trp Leu
65 70 75 80

Leu Leu Thr Leu Ser Asp Glu Val Thr Pro Ala Asn Val Ser Ser Val
85 90 95

Thr Pro Ile His Leu Leu Val Leu Leu Tyr Trp Gly Ile Ala Val Ile
 100 105 110

Ala Thr Ala Leu Ser Pro Val Lys Lys Ala Ala Leu Asn Asp Leu Gly
 115 120 125

Thr Leu Thr Leu Tyr Leu Leu Leu Phe Ala Leu Cys Ala Arg Val Leu
 130 135 140

Arg Ser Pro Arg Leu Arg Ser Trp Ile Leu Thr Leu Tyr Leu His Val
 145 150 155 160

Ser Leu Ile Val Ser Val Tyr Gly Leu Arg Gln Trp Phe Phe Gly Ala
 165 170 175

Thr Ala Leu Ala Thr Trp Val Asp Pro Glu Ser Pro Leu Ser Lys Thr
 180 185 190

Thr Arg Val Tyr Ser Tyr Leu Gly Asn Pro Asn Leu Leu Ala Gly Tyr
 195 200 205

Leu Leu Pro Ala Val Ile Phe Ser Leu Val Ala Ile Phe Ala Trp Gln
 210 215 220

Ser Trp Leu Lys Lys Ala Leu Ala Leu Thr Met Leu Ile Val Asn Thr
 225 230 235 240

Ala Cys Leu Ile Leu Thr Phe Ser Arg Gly Gly Trp Ile Gly Leu Val
 245 250 255

Val Ala Val Leu Ala Val Met Ala Leu Leu Val Phe Trp Lys Ser Val
 260 265 270

Glu Met Pro Pro Phe Trp Arg Thr Trp Ser Leu Pro Ile Val Leu Gly
 275 280 285

Gly Leu Ile Gly Ile Leu Leu Leu Ala Val Ile Phe Val Glu Pro Val
 290 295 300

Arg Leu Arg Val Phe Ser Ile Phe Ala Asp Arg Gln Asp Ser Ser Asn
 305 310 315 320

Asn Phe Arg Arg Asn Val Trp Asp Ala Val Phe Glu Met Ile Arg Asp
 325 330 335

Arg Pro Ile Phe Gly Ile Gly Pro Gly His Asn Ser Phe Asn Lys Val
 340 345 350

Tyr Pro Leu Tyr Gln His Pro Arg Tyr Thr Ala Leu Ser Ala Tyr Ser
 355 360 365

Ile Leu Phe Glu Val Thr Val Glu Thr Gly Phe Val Gly Leu Ala Cys
 370 375 380

Phe Leu Trp Leu Ile Ile Val Thr Phe Asn Thr Ala Leu Leu Gln Val
 385 390 395 400

Arg Arg Leu Arg Arg Leu Arg Ser Val Glu Gly Phe Trp Leu Ile Gly
 405 410 415

Ala Ile Ala Ile Leu Leu Gly Met Leu Ala His Gly Thr Val Asp Thr
 420 425 430

Val Trp Tyr Arg Pro Glu Val Asn Thr Leu Trp Trp Leu Ile Val Ala
 435 440 445

Leu Ile Ala Ser Tyr Trp Thr Pro Leu Thr Gln Asn Gln Thr Asn Pro
 450 455 460

Ser Asn Pro Glu Pro Ala Val Asn
 465 470

<210> 8
 <211> 1425
 <212> DNA
 <213> Anabaena PCC7120

<400> 8
 atgaatttag tctggcaacg atttacttta tcttctttac ctctaaaaca gtttctagct 60
 acaagttact tacatcggtt cctagtggga ctgttatctt cttggcggca aactagtttc 120
 ttacttcagt ggggagacat gattgcagct gcgttactca gcttgatata tgttttggt 180
 ccctttgtct ctagtactct cgttggtgtg ctgctgatag cttgtgtagg tttttggtta 240
 ttgttgactt tatctgatga accttcatca aacaataact cccttggtac tcccatcac 300
 ctgttggtgt tgctctattg gggaattgct gctgtagcaa cggcattatc accagtcaag 360
 aaggcagcat taactgattt gttaaccttg actttgtatt tgctactatt tgctctttgt 420
 gccaggggtc tgagatcgcc gcgtctgagg tcttgatca ttacctcta cctatctgca 480
 tcaactggtg tcagtatata tggaatgcga caatggcggt ttggtgcgcc cccactggcg 540
 acttgggttg atccagagtc caccttgtct aaaaccacaa gggtttacag ttatttaggc 600
 aatcccaatt tgttggtctg ttatttagta ccggcgggtga tttttagcct catggcagtt 660
 tttgtctggc agggctgggc aagaaaatct ttagctgtaa caatgctgtt tgtaaact 720
 gcttgctaa tttttactta tagtcgtggc ggctggattg gtcttgtggt agcagctcta 780
 ggggcgacgg cattgctagt tgattggtg agtgtgcaaa tgccgccttt ttggcgaacc 840
 tggtcattac ccatactttt gggcgggttg atcggggtat tgttgattgc ggtgttattt 900
 gtcgagccag tccggtttcg agttctcagt atttttgccg atcgccaaga tagcagcaat 960
 aattttcgcc gcaacgtgtg ggatgctgtt tttgagatga tccgcgatcg cccaattatt 1020
 ggtattggcc ctggtcataa ttcttttaaat aaagtctacc ctctttacca aagacctcgt 1080
 tatagtgtt taagtgccta ttccatcttc ctagaggtgg ctgtagaaat gggttttgtt 1140
 ggactagctt gctttctctg gttaattatc gtcactatta atacagcatt cgttcagcta 1200
 cgccaactgc gccaatctgc caatgtgcaa ggatttttgt tgggtgggtgc cttagccaca 1260
 ttgctgggaa tgctggctca cggtagcgtg gacactatat ggtttcgtcc ggaagtaaat 1320
 actcttttgt ggtaaatggt tgctctcatt gctagctatt ggacaccttt atccgcaaac 1380
 caatgtcaag aactcaattt atttaaggaa gaaccacaaa gcaac 1425

<210> 9
 <211> 1419
 <212> DNA
 <213> Nostoc punctiforme

<400> 9

```

atgaatttag tctggcaact atttacttta tcatctttac cgctcaaaga atatcttgct 60
accagttacg tacaccgttc tctggtggga ctgttaagct cttggcggca aaccagcgtc 120
ttgattcagt ggggagatgc gatagcagct gtattactca gctcaatata tgcccttgca 180
ccttttgctt cgagtacttt ggtaggttta ttgctggtcg cttgtgtggg attttggcta 240
ttgttgactt tatctgatga agtcacacca gcaaatgtct cgtcagtcac tccattcat 300
ctactgggat tgctctactg gggaattgcc gtaatcgcaa cagcattatc accagtgaag 360
aaagcggcac ttaacgactt gggaactttg accttgattt tgctactatt tgccctttgt 420
gccaggggat taaggctgcc tcgcctccgg tcttggtatc tcacccttta tetgcacgta 480
tcgttaattg tcagtgtcta tggattgcgg caatggtttt ttggagccac agcactggca 540
acttgggttg atccggaatc tcctctgtct aagactacaa gagtctacag ttatttagga 600
aatcccaact tattggctgg atacctctta ccagcagtaa tttttagctt ggtggcaatt 660
tttgcatggc aaagttggct caaaaaagcc ttagcattaa caatgttgat tgtcaatact 720
gcctgcctga tcctgacttt tagtcgtggc gggttgattg gactagtggg ggcagttttg 780
gcggtgatgg cattgctagt tttttggaag agtgtggaaa tgcctccttt ttggcgtagt 840
tggtcgctgc ccattgtctt aggaggttta attgggatat tactgttagc agtgatattt 900
gtagagccag ttcgcctgcg ggtgttcagc atttttgctg accgtcaaga tagtagtaat 960
aattttcgtc gaaatgtgtg ggatgctgtc tttagatga ttcgcgatcg cccaattttc 1020
ggatttggcc ctggtcacaa ctcttttaat aaagtttatc cgctctacca acaccctcgg 1080
tacactgctt taagtgttta ttcgattttg ttgaagtga ctgtagaaac tgggtttggt 1140
ggtttagctt gctttctctg gctaataatc gtcacattta atacggcgct ttgcaagta 1200
cgacgattgc gacgattgag aagtgtagag ggattttggt taattggagc gatcgctatt 1260
ttgttgggta tgctcgctca cggcactgta gatactgtct ggtatcgcc tgaagtcaat 1320
accctctggt ggctcatcgt tgctttaatt gccagctact ggacaccttt aactcaaaac 1380
cagacaaatc catctaacc agaacagca gtaactaa 1419

```

```

<210> 10
<211> 461
<212> PRT
<213> Trichodesmium erythraeum

```

```

<400> 10

```

```

Met Asn Ser Val Trp Lys Lys Leu Thr Leu Thr Asn Leu Ser Phe Ser
1          5          10          15

```

```

Asp Ser Glu Trp Leu Asn Ala Ser Tyr Leu Tyr Gly Leu Leu Asn Gly
20          25          30

```

```

Ser Leu Tyr Asn Trp Arg Arg Gly Ser Trp Leu Met Gln Trp Gly Glu
35          40          45

```

```

Pro Leu Gly Phe Val Leu Leu Ala Ile Val Phe Thr Leu Ala Pro Phe
50          55          60

```

```

Val Asn Thr Thr Leu Ile Gly Phe Leu Leu Leu Ala Ser Ala Gly Phe
65          70          75          80

```

```

Trp Val Leu Leu Lys Val Ser Asp Asn Thr Gln Glu Tyr Leu Thr Pro
85          90          95

```

Ile His Leu Leu Ile Phe Leu Tyr Trp Ser Ile Ala Thr Leu Ala Val
 100 105 110

Val Ile Ser Pro Ala Lys Thr Ala Ala Phe Ser Gly Trp Val Lys Leu
 115 120 125

Thr Leu Tyr Leu Leu Leu Phe Ala Ser Gly Ser Leu Val Leu Arg Ser
 130 135 140

Pro Arg Leu Arg Ser Trp Leu Ile Asn Ile Tyr Leu Leu Val Ser Leu
 145 150 155 160

Val Val Ser Phe Tyr Gly Ile Arg Gln Trp Ile Asp Lys Val Glu Pro
 165 170 175

Leu Ala Thr Trp Asn Asp Pro Thr Ser Ala Gln Ala Gly Ala Thr Arg
 180 185 190

Val Tyr Ser Tyr Leu Gly Asn Pro Asn Leu Leu Gly Gly Tyr Leu Leu
 195 200 205

Pro Ala Ile Ala Leu Ser Phe Val Ala Ile Phe Ala Trp Ser Ser Trp
 210 215 220

Ala Arg Lys Ser Leu Ala Val Thr Ile Leu Leu Val Ser Cys Ala Cys
 225 230 235 240

Leu Arg Tyr Thr Gly Ser Arg Gly Ser Trp Ile Gly Phe Leu Ala Leu
 245 250 255

Met Phe Ala Met Leu Ile Leu Met Trp Tyr Trp Trp Arg Ser Tyr Met
 260 265 270

Pro Ser Phe Trp Gln Ile Trp Ser Leu Pro Ile Ala Val Gly Ser Phe
 275 280 285

Ala Gly Leu Leu Ile Leu Ala Val Val Leu Leu Glu Pro Leu Arg Asp
 290 295 300

Arg Val Leu Ser Val Phe Ala Gly Arg Gln Asp Ser Ser Asn Asn Phe
 305 310 315 320

Arg Met Asn Val Trp Met Ser Val Phe Asp Met Ile Arg Asp Arg Pro
 325 330 335

Ile Leu Gly Ile Gly Pro Gly Asn Asp Val Phe Asn Lys Ile Tyr Pro
 340 345 350

Leu Tyr Gln Arg Pro Arg Tyr Ser Ala Leu Ser Ser Tyr Ser Val Pro
 355 360 365

Leu Glu Ile Val Val Glu Thr Gly Phe Ile Gly Leu Thr Ala Phe Leu
 370 375 380

Trp Leu Leu Leu Val Thr Phe Asn Gln Gly Val Leu Gln Leu Lys Arg
 385 390 395 400

Leu Arg Asp Ala Asp Asn Pro Gln Gly Tyr Trp Leu Ile Gly Ala Ile
 405 410 415

Ala Ala Met Val Gly Leu Ile Gly His Gly Leu Val Asp Thr Val Trp
420 425 430

Tyr Arg Pro Gln Val Asn Thr Ile Trp Trp Leu Met Val Ala Ile Ile
435 440 445

Ala Ser Tyr Ser Ser Gln Gln Gly Val Arg Ser Arg Glu
450 455 460

<210> 11
<211> 463
<212> PRT
<213> Thermosynechococcus elongatus BP-1

<400> 11

Met Asp Val Leu Leu Arg Arg Leu Asp Val Glu Gly Trp Arg Ser His
1 5 10 15

Ser Gly Val Gly Arg Leu Leu Gly Leu Leu Gln Gly Trp Gln Glu Lys
20 25 30

Ser Trp Leu Gly Arg Trp Leu Pro Ser Leu Ala Val Leu Leu Val Gly
35 40 45

Leu Val Leu Val Leu Ala Pro Leu Met Pro Ser Gly Met Ile Gly Met
50 55 60

Leu Leu Ala Ala Gly Ser Gly Phe Trp Leu Leu Trp Thr Leu Ala Gly
65 70 75 80

Glu Arg Glu Gly Arg Trp Ser Gly Val His Leu Leu Val Leu Leu Tyr
85 90 95

Trp Gly Ile Ala Leu Leu Ala Thr Val Leu Ser Pro Val Pro Arg Ala
100 105 110

Ala Met Val Gly Leu Gly Lys Leu Thr Leu Tyr Leu Leu Phe Phe Ala
115 120 125

Leu Ala Glu Arg Val Met Arg Asn Glu Arg Trp Arg Ser Arg Leu Leu
130 135 140

Thr Val Tyr Leu Leu Thr Ala Leu Met Val Ser Val Glu Gly Val Arg
145 150 155 160

Gln Trp Ile Phe Gly Ala Glu Pro Leu Ala Thr Trp Thr Asp Pro Glu
165 170 175

Ser Ala Leu Ala Asn Val Thr Arg Val Tyr Ser Phe Leu Gly Asn Pro
180 185 190

Asn Leu Leu Ala Gly Tyr Leu Leu Pro Ser Val Pro Leu Ser Ala Ala
195 200 205

Ala Ile Ala Val Trp Gln Gly Trp Leu Pro Lys Leu Leu Ala Val Val
210 215 220

Met Leu Gly Met Asn Ala Ala Ser Leu Ile Leu Thr Phe Ser Arg Gly
225 230 235 240

Gly Trp Leu Gly Leu Val Ala Ala Thr Ile Ala Gly Val Val Leu Leu
245 250 255

Gly Ile Trp Phe Trp Pro Arg Leu Pro Leu Gln Trp Arg Arg Trp Gly
260 265 270

Val Pro Thr Met Gly Gly Leu Ala Ile Ala Leu Cys Met Gly Thr Ile
275 280 285

Val Ser Val Pro Pro Leu Arg Glu Arg Ala Ala Ser Ile Phe Val Ala
290 295 300

Arg Gly Asp Ser Ser Asn Asn Phe Arg Ile Asn Val Trp Met Ala Val
305 310 315 320

Gln Gln Met Ile Trp Ala Arg Pro Trp Leu Gly Ile Gly Pro Gly Asn
325 330 335

Val Ala Phe Asn Gln Ile Tyr Pro Leu Tyr Gln Val Asn Val Arg Phe
340 345 350

Thr Ala Leu Gly Ala Tyr Ser Ile Phe Leu Glu Ile Leu Val Glu Val
355 360 365

Gly Phe Ile Gly Phe Gly Val Phe Leu Trp Leu Leu Ala Val Leu Gly
370 375 380

Asp Arg Ala Arg Arg Cys Phe Glu Glu Leu Arg Ala Thr Gly Ser Pro
385 390 395 400

Gln Gly Phe Trp Leu Met Gly Thr Ile Ala Ala Met Ile Gly Met Leu
405 410 415

Thr His Gly Leu Val Asp Thr Ile Trp Phe Arg Pro Glu Val Ala Thr
420 425 430

Leu Trp Trp Leu Met Val Ala Ile Val Ala Ser Phe Thr Pro Phe Gln
435 440 445

Ser Lys Thr Ala Asn Gly Thr Phe Ser Asn Arg Asp Pro Glu Pro
450 455 460

<210> 12
<211> 439
<212> PRT
<213> Prochlorococcus marinus

<400> 12

Met Pro Lys Thr Ala Ala Pro Gln Pro Leu Leu Arg Trp Gln Gly
1 5 10 15

His Ile Pro Ser Ser Glu Ala Met Gln Met Arg Leu Gln Trp Ile Ala
20 25 30

Gly Leu Leu Leu Met Met Leu Leu Ala Thr Leu Pro Met Leu Thr Arg
35 40 45

Thr Gly Leu Gly Leu Thr Ile Leu Ala Ala Gly Ala Leu Trp Ile Ile
50 55 60

Trp Gly Cys Val Thr Pro Ala Gly Arg Ile Gly Ser Ile Ser Ser Cys
 65 70 75 80
 Leu Leu Val Phe Phe Ala Ile Ala Cys Leu Ala Thr Gly Phe Ser Pro
 85 90 95
 Val Pro Leu Ala Ala Ala Lys Gly Leu Ile Lys Leu Ile Ser Tyr Leu
 100 105 110
 Gly Val Tyr Ala Leu Met Arg Gln Leu Leu Ala Thr Ser Ser Asp Trp
 115 120 125
 Trp Asp Arg Leu Val Ala Ala Leu Leu Thr Gly Glu Leu Ile Ser Ser
 130 135 140
 Val Ile Ala Ile Arg Gln Leu Tyr Ala Pro Ala Glu Glu Met Ala His
 145 150 155 160
 Trp Ala Asp Pro Asn Ser Val Ala Ala Gly Thr Val Arg Ile Tyr Gly
 165 170 175
 Pro Leu Gly Asn Pro Asn Leu Leu Ala Gly Tyr Leu Met Pro Ile Leu
 180 185 190
 Pro Leu Ala Leu Val Ala Leu Leu Arg Trp Gln Gly Leu Gly Ala Lys
 195 200 205
 Leu Tyr Ala Met Val Ala Leu Gly Leu Gly Ile Thr Ala Thr Leu Phe
 210 215 220
 Ser Phe Ser Arg Gly Gly Trp Leu Gly Met Leu Ser Ala Leu Ala Val
 225 230 235 240
 Ile Leu Val Leu Leu Leu Leu Arg Ser Thr Ser His Trp Pro Leu Val
 245 250 255
 Trp Arg Arg Leu Leu Pro Leu Ile Val Ile Val Leu Gly Thr Ala Met
 260 265 270
 Leu Val Ile Ala Ala Thr Gln Ile Glu Pro Ile Arg Thr Arg Ile Thr
 275 280 285
 Ser Leu Ile Ala Gly Arg Ser Asp Ser Ser Asn Asn Phe Arg Ile Asn
 290 295 300
 Val Trp Leu Ser Ser Leu Glu Met Ile Gln Ala Arg Pro Trp Leu Gly
 305 310 315 320
 Ile Gly Pro Gly Asn Ala Ala Phe Asn Arg Ile Tyr Pro Leu Phe Gln
 325 330 335
 Gln Pro Lys Phe Asn Ala Leu Ser Ala Tyr Ser Val Pro Leu Glu Ile
 340 345 350
 Leu Val Glu Thr Gly Leu Ala Gly Leu Met Ala Ser Leu Ala Leu Val
 355 360 365
 Ile Thr Gly Met Arg Lys Gly Leu Ala Gly Leu Asn Ser Asn His Pro

370

375

380

Leu Ala Leu Pro Ala Leu Ala Ser Leu Ala Ala Ile Ala Gly Leu Ala
 385 390 395 400

Val His Gly Ile Thr Asp Thr Ile Phe Phe Arg Pro Glu Val Gln Leu
 405 410 415

Val Gly Trp Phe Cys Leu Ala Thr Leu Ala Gln Thr Gln Pro Glu Gln
 420 425 430

Lys Gln Leu Gln Gln Thr Glu
 435

<210> 13
 <211> 431
 <212> PRT
 <213> Synechococcus WH 8102

<400> 13

Met Ala Asp Ala Thr Asp Gln Arg Ser Ile Pro Leu Leu Leu Arg Trp
 1 5 10 15

Gln Gly Cys Leu Thr Pro Thr Ala Ser Val Gln Gln Arg Leu Glu Leu
 20 25 30

Leu Ser Gly Val Val Leu Met Leu Leu Leu Gly Ser Leu Pro Phe Val
 35 40 45

Ser Arg Ser Gly Leu Gly Leu Glu Leu Ala Ala Ala Gly Leu Leu Trp
 50 55 60

Leu Leu Trp Ser Leu Ile Thr Pro Ala Lys Arg Leu Gly Ala Ile Ser
 65 70 75 80

Arg Trp Val Leu Leu Tyr Leu Ala Ile Ala Trp Val Cys Thr Gly Phe
 85 90 95

Ser Pro Val Pro Ile Ala Ala Ala Lys Gly Leu Leu Lys Leu Thr Ser
 100 105 110

Tyr Leu Gly Val Tyr Ala Leu Met Arg Thr Leu Leu Glu Arg Gln Ile
 115 120 125

Val Trp Trp Asp Arg Leu Leu Ala Ala Leu Leu Gly Gly Gly Leu Phe
 130 135 140

Ser Ser Val Leu Ala Leu Arg Gln Leu Tyr Ala Ser Thr Asp Glu Leu
 145 150 155 160

Ala Gly Trp Ala Asp Pro Asn Ser Val Ser Ala Gly Thr Ile Arg Ile
 165 170 175

Tyr Gly Pro Leu Gly Asn Pro Asn Leu Leu Ala Gly Tyr Leu Leu Pro
 180 185 190

Leu Val Pro Leu Ala Cys Ile Ala Val Leu Arg Trp Lys Arg Leu Ser
 195 200 205

Cys Arg Leu Leu Ala Ala Val Thr Ala Leu Leu Ala Gly Ser Ala Thr

210	215	220
Val Phe Thr Tyr Ser Arg Gly Gly Trp Leu Gly Leu Leu Ala Ala Leu 225 230 235 240		
Ala Leu Ala Gly Met Leu Ile Leu Leu Arg Thr Thr Ala His Trp Pro 245 250 255		
Pro Leu Trp Arg Arg Leu Leu Pro Leu Ala Ala Leu Leu Ile Ala Gly 260 265 270		
Ile Ala Leu Ala Leu Ala Ile Thr Gln Leu Asp Pro Ile Arg Thr Arg 275 280 285		
Val Leu Ser Leu Val Ala Gly Arg Gly Asp Ser Ser Asn Asn Phe Arg 290 295 300		
Ile Asn Val Trp Leu Ala Ala Ile Glu Met Val Gln Asp Arg Pro Trp 305 310 315 320		
Leu Gly Ile Gly Pro Gly Asn Ala Ala Phe Asn Ser Ile Tyr Pro Leu 325 330 335		
Tyr Gln Gln Pro Lys Phe Asp Ala Leu Ser Ala Tyr Ser Val Pro Leu 340 345 350		
Glu Ile Leu Val Glu Thr Gly Ile Pro Gly Leu Leu Ala Cys Leu Gly 355 360 365		
Leu Leu Leu Ser Ser Ile Gln Arg Gly Leu Arg Ile His Gly Gln Gln 370 375 380		
Gly Leu Ile Ala Ile Gly Ser Leu Ala Ala Ile Ala Gly Leu Leu Thr 385 390 395 400		
Gln Gly Ile Thr Asp Thr Ile Phe Phe Arg Pro Glu Val Gln Leu Ile 405 410 415		
Gly Trp Phe Ala Leu Ala Ser Leu Gly Ala Thr Trp Leu Arg Asp 420 425 430		